

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	3	Leppert.in. and Singh.in. and Charlier.in.	US-PGPUB; USPAT; USOCR; DERWENT	OR	ON	2005/08/30 13:19
S1	21	Aiyar.in.	US-PGPUB; USPAT; USOCR; DERWENT	OR	ON	2005/08/30 13:18
S2	45	Iannotti.in.	US-PGPUB; USPAT; USOCR; DERWENT	OR	ON	2005/08/30 13:03
S3	2319	Christian.in. and potassium	US-PGPUB; USPAT; USOCR; DERWENT	OR	ON	2005/08/30 13:04
S4	25765	Christian.in.	US-PGPUB; USPAT; USOCR; DERWENT	OR	ON	2005/08/30 13:04
S5	375	Logsdon.in.	US-PGPUB; USPAT; USOCR; DERWENT	OR	ON	2005/08/30 13:04

09/209,125

FILE 'HOME' ENTERED AT 16:06:06 ON 30 AUG 2005

=> FILE SCISEARCH, MEDLINE, CAPLUS, BIOSIS, EMBASE

=> S AIYAR

L1 63 AIYAR

=> S IANNOTTI

L2 7 IANNOTTI

=> S CHRISTIAN, EDWARD P OR CHRISTIAN, EP OR CHRISTIAN E

L3 6 CHRISTIAN, EDWARD P OR CHRISTIAN, EP OR CHRISTIAN E

=> S CHRISTIAN

L4 8583 CHRISTIAN

=> S POTASSIUM

L5 1204230 POTASSIUM

=> S L6 AND L7

L6 37 L6 AND L7

=> S LOGSDON

L7 52 LOGSDON

09/209,125 Results

SEQ ID NO: 2 oligo. search

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2565	100.0	2565	6	A94975	A94975 Sequence 2
2	2565	100.0	2565	6	BD136514	BD136514 Human bra
3	2565	100.0	3195	9	AF074247	AF074247 Homo sapi
4	2444	95.3	3029	6	A94974	A94974 Sequence 1
5	2444	95.3	3029	6	BD136513	BD136513 Human bra
6	1709	66.6	1878	6	CQ754328	CQ754328 Sequence
7	1709	66.6	1878	6	CQ754458	CQ754458 Sequence
8	1420	55.4	7420	9	HSKCNQ2	Y15065 Homo sapien
9	1269	49.5	3232	6	AR216854	AR216854 Sequence
10	1269	49.5	3232	6	BD086323	BD086323 KCNQ2 and
11	1269	49.5	3232	9	AF033348	AF033348 Homo sapi
12	1259	49.1	3237	6	AR216941	AR216941 Sequence
13	1259	49.1	3237	6	BD086411	BD086411 KCNQ2 and
14	1247	48.6	1932	6	CQ754326	CQ754326 Sequence
15	1247	48.6	1932	6	CQ754456	CQ754456 Sequence

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2565	100.0	2565	2	AAX81548	Aax81548 Human bra
2	2565	100.0	3195	5	AAS74831	Aas74831 DNA encod
3	2444	95.3	3029	2	AAX81547	Aax81547 Human bra
4	1709	66.6	1878	12	ADH51117	Adh51117 Potassium
5	1709	66.6	1878	12	ADM77993	Adm77993 KCNQ2-15b
6	1677	65.4	4512	10	ADJ56528	Adj56528 Rat cDNA
7	1420	55.4	7407	10	ADB78685	Adb78685 Human pot
8	1420	55.4	7411	10	ADD29557	Add29557 Human tum
9	1420	55.4	7420	11	ADN38963	Adn38963 Cancer/an
10	1420	55.4	7420	11	ADP65810	Adp65810 Human mRN
11	1420	55.4	7420	11	ADP65731	Adp65731 Human pot
12	1420	55.4	7420	12	ADL06495	Adl06495 Human tum
13	1420	55.4	7863	10	ADJ56529	Adj56529 Human cDN
14	1369	53.4	7407	10	ADB78688	Adb78688 Human pot
15	1369	53.4	7407	10	ADB78686	Adb78686 Human pot

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1709	66.6	1878	20	US-10-744-796-3	Sequence 3, Appli
2	1677	65.4	4512	15	US-10-084-817-334	Sequence 334, App
3	1420	55.4	7407	21	US-10-482-834A-56	Sequence 56, Appli
4	1420	55.4	7411	20	US-10-335-053-6	Sequence 6, Appli
5	1420	55.4	7420	17	US-10-295-027-281	Sequence 281, App
6	1420	55.4	7420	20	US-10-643-795A-75	Sequence 75, Appli
7	1420	55.4	7420	21	US-10-948-518-75	Sequence 75, Appli
8	1420	55.4	7863	15	US-10-084-817-335	Sequence 335, App
9	1369	53.4	7407	21	US-10-482-834A-54	Sequence 54, Appli
10	1369	53.4	7407	21	US-10-482-834A-57	Sequence 57, Appli
11	1369	53.4	7407	21	US-10-482-834A-58	Sequence 58, Appli
12	1369	53.4	7407	21	US-10-482-834A-59	Sequence 59, Appli
13	1269	49.5	2619	15	US-10-345-680-18	Sequence 18, Appli
14	1269	49.5	3232	15	US-10-345-680-16	Sequence 16, Appli
15	1269	49.5	3232	16	US-10-096-578-1	Sequence 1, Appli

RESULT 15
US-10-096-578-1

; Sequence 1, Application US/10096578
; Publication No. US20030165874A1
; GENERAL INFORMATION:
; APPLICANT: Luppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-160
; CURRENT APPLICATION NUMBER: US/10/096,578
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 09/177,650
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/063,147
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2743)
; NAME/KEY: mutation
; LOCATION: (975)..(976)
; OTHER INFORMATION: There is an insertion of a GT between nucleotides
; OTHER INFORMATION: 975 and 976 in kindred K1504.
; NAME/KEY: mutation
; LOCATION: (978)
; OTHER INFORMATION: The mutation A to G occurs at this base in kindred
; OTHER INFORMATION: K3904.
; NAME/KEY: mutation
; LOCATION: (1043)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K1705.
; NAME/KEY: mutation
; LOCATION: (1691)..(1703)
; OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
; OTHER INFORMATION: deleted in kindred K3369.
; NAME/KEY: allele
; LOCATION: (1039)
; OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
; OTHER INFORMATION: the control population.
; NAME/KEY: allele
; LOCATION: (1846)
; OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
; OTHER INFORMATION: the control population.
; NAME/KEY: mutation
; LOCATION: (1469)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K1525.
; NAME/KEY: mutation
; LOCATION: (1094)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K4443.
; NAME/KEY: mutation
; LOCATION: (1125)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K4516.
; NAME/KEY: mutation
; LOCATION: (2736)..(2737)
; OTHER INFORMATION: There is an insertion of GGGCC between these two
; OTHER INFORMATION: nucleotides in K3963.
US-10-096-578-1

Query Match 49.5%; Score 1269; DB 16; Length 3232;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1246	AGCCAGAAGGTCA GTT GAAAGATCGTCTTCTCCAGCCCCGAGGC GTGGCTGCCAAG	1305
Db	1427	AGCCAGAAGGTCA GTT GAAAGATCGTCTTCTCCAGCCCCGAGGC GTGGCTGCCAAG	1486
Qy	1306	GGGAAGGGTCCCGCAGGCCAGACTGTGAGGCCGTACCCAGCGCCGACCAGAGCCTC	1365
Db	1487	GGGAAGGGTCCCGCAGGCCAGACTGTGAGGCCGTACCCAGCGCCGACCAGAGCCTC	1546
Qy	1366	GAGGACAGCCCAGCAAGGTGCCAAGAGCTGGAGCTTCGGGACCGCAGCCGGCACGC	1425
Db	1547	GAGGACAGCCCAGCAAGGTGCCAAGAGCTGGAGCTTCGGGACCGCAGCCGGCACGC	1606
Qy	1426	CAGGCTTCCGCATCAAGGTGCCGTACGGCAGAACTCAGAAGAAGCAAGCCTCCC	1485
Db	1607	CAGGCTTCCGCATCAAGGTGCCGTACGGCAGAACTCAGAAGAAGCAAGCCTCCC	1666
Qy	1486	GGAGAGGACATTGTGGATGACAAGAGCTGCCCTGCGAGTTGTGACCGAGGACCTGACC	1545
Db	1667	GGAGAGGACATTGTGGATGACAAGAGCTGCCCTGCGAGTTGTGACCGAGGACCTGACC	1726
Qy	1546	CCGGCCTCAAAGTCAGCATCAGAGCGTGTGTCA TGCGGTTCTGGTGTCCAAGCGG	1605
Db	1727	CCGGCCTCAAAGTCAGCATCAGAGCGTGTGTCA TGCGGTTCTGGTGTCCAAGCGG	1786
Qy	1606	AAGTTCAAGGAGAGCCTGCCCTACGACGTGATGGACGTCATCGAGCAGTACTCAGCC	1665
Db	1787	AAGTTCAAGGAGAGCCTGCCCTACGACGTGATGGACGTCATCGAGCAGTACTCAGCC	1846
Qy	1666	GGCCACCTGGACATGCTGCCGAATTAGAGCCTGCAGTCCAGAGTGGACCAGATCGT	1725
Db	1847	GGCCACCTGGACATGCTGCCGAATTAGAGCCTGCAGTCCAGAGTGGACCAGATCGT	1906
Qy	1726	GGCGGGGCCAGCGATCACCGACAAGGACCGCACCAGGGCCCGCCGAGGCGGAGCTG	1785
Db	1907	GGCGGGGCCAGCGATCACCGACAAGGACCGCACCAGGGCCCGCCGAGGCGGAGCTG	1966
Qy	1786	CCCGAGGACCCAGCATGATGGACGGCTCGGAAGGTGGAGAACAGGTCTTGTCCATG	1845
Db	1967	CCCGAGGACCCAGCATGATGGACGGCTCGGAAGGTGGAGAACAGGTCTTGTCCATG	2026
Qy	1846	GAGAAGAAGCTGGACTTCTGGTAATATCTACATGCAGCGGATGGCATCCCCCGACA	1905
Db	2027	GAGAAGAAGCTGGACTTCTGGTAATATCTACATGCAGCGGATGGCATCCCCCGACA	2086
Qy	1906	GAGACCGAGGCCTACTTGGGCAAAAGAGCGGAGCCGGCGCCCGTACACAGCCCG	1965
Db	2087	GAGACCGAGGCCTACTTGGGCAAAAGAGCGGAGCCGGCGCCCGTACACAGCCCG	2146
Qy	1966	GAAGACAGCGGGAGCATGTCGACAGGCACGGCTGCATTGTCAAGATCGTGCCTCCAGC	2025
Db	2147	GAAGACAGCGGGAGCATGTCGACAGGCACGGCTGCATTGTCAAGATCGTGCCTCCAGC	2206
Qy	2026	AGCTCCACGGGCCAGAAGAACCTCTCGGCCCGCCCGCGCCCGTCCAGTGTCCG	2085
Db	2207	AGCTCCACGGGCCAGAAGAACCTCTCGGCCCGCCCGCGCCCGTCCAGTGTCCG	2266
Qy	2086	CCCTCCACCTCTGGCAGCCACAGAGCCACCCGCCAGGCCACGGCACCTCCCCGTG	2145
Db	2267	CCCTCCACCTCTGGCAGCCACAGAGCCACCCGCCAGGCCACGGCACCTCCCCGTG	2326
Qy	2146	GGGGACCACGGCTCCCTGGTGCATCCGCCCGCCGTCCACAGAGCGGTGCGCTGTCC	2205
Db	2327	GGGGACCACGGCTCCCTGGTGCATCCGCCCGCCGTCCACAGAGCGGTGCGCTGTCC	2386
Qy	2206	GCCTACGGCGGGCAACCGCGCAGCATGGAGTTCTGCGGCAGGAGGACACCCGGGC	2265
Db	2387	GCCTACGGCGGGCAACCGCGCAGCATGGAGTTCTGCGGCAGGAGGACACCCGGGC	2446
Qy	2266	TGCAGGCCCGAGGGACCTGCCGGACAGCGACACGTCCATCTCCATCCGTCCGTG	2325
Db	2447	TGCAGGCCCGAGGGACCTGCCGGACAGCGACACGTCCATCTCCATCCGTCCGTG	2506

Qy	2326 GACCACGAGGAGCTGGAGCGTCCTTCAGCGGCTTCAGCATCTCCAGTCCAAGGAGAAC	2385
Db	2507 GACCACGAGGAGCTGGAGCGTCCTTCAGCGGCTTCAGCATCTCCAGTCCAAGGAGAAC	2566
Qy	2386 CTGGATGCTCTAACAGCTGCTACGCGGCCGTGGCGCCTTGTGCCAAGTCAGGCCCTAC	2445
Db	2567 CTGGATGCTCTAACAGCTGCTACGCGGCCGTGGCGCCTTGTGCCAAGTCAGGCCCTAC	2626
Qy	2446 ATTGCGGAGGGAGAGTCAGACACCGACTCCGACCTCTGTACCCGTGCGGGCCCCGCCA	2505
Db	2627 ATTGCGGAGGGAGAGTCAGACACCGACTCCGACCTCTGTACCCGTGCGGGCCCCGCCA	2686
Qy	2506 CGCTCGGCCACCGCGAGGGTCCCTTGGTGACGTGGCTGGCCGGGCCAGGAAGTGA	2565
Db	2687 CGCTCGGCCACCGCGAGGGTCCCTTGGTGACGTGGCTGGCCGGGCCAGGAAGTGA	2746

SUMMARIES

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Result	Query				Description
No.	Score	Match	Length	DB	ID
1	2565	100.0	2565	6	A94975
2	2565	100.0	2565	6	BD136514
3	2565	100.0	3195	9	AF074247
4	2553	99.5	3029	6	A94974
5	2553	99.5	3029	6	BD136513
6	2499.4	97.4	3232	6	AR216854
7	2499.4	97.4	3232	6	BD086323
8	2499	97.4	3232	9	AF033348
9	2495	97.3	7420	9	HSKCNQ2
10	2489.4	97.1	3237	6	AR216941
11	2489.4	97.1	3237	6	BD086411
12	2480.2	96.7	3287	6	AR213254
13	2480.2	96.7	3287	6	BD074165
14	2455.8	95.7	2750	6	AX456861
15	2455.8	95.7	2750	9	AF110020

09/209,125 Results

SEQ ID NO: 2

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2565	100.0	2565	6	A94975	A94975 Sequence 2
2	2565	100.0	2565	6	BD136514	BD136514 Human bra
3	2565	100.0	3195	9	AF074247	AF074247 Homo sapi
4	2553	99.5	3029	6	A94974	A94974 Sequence 1
5	2553	99.5	3029	6	BD136513	BD136513 Human bra
6	2499.4	97.4	3232	6	AR216854	AR216854 Sequence
7	2499.4	97.4	3232	6	BD086323	BD086323 KCNQ2 and
8	2499	97.4	3232	9	AF033348	AF033348 Homo sapi
9	2495	97.3	7420	9	HSKCNQ2	Y15065 Homo sapien
10	2489.4	97.1	3237	6	AR216941	AR216941 Sequence
11	2489.4	97.1	3237	6	BD086411	BD086411 KCNQ2 and
12	2480.2	96.7	3287	6	AR213254	AR213254 Sequence
13	2480.2	96.7	3287	6	BD074165	BD074165 KCNQ pota
14	2455.8	95.7	2750	6	AX456861	AX456861 Sequence
15	2455.8	95.7	2750	9	AF110020	AF110020 Homo sapi

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2565	100.0	2565	2	AAX81548	Aax81548 Human bra
2	2565	100.0	3195	5	AAS74831	Aas74831 DNA encod
3	2553	99.5	3029	2	AAX81547	Aax81547 Human bra
4	2506.4	97.7	4512	10	ADJ56528	Adj56528 Rat cDNA
5	2499.4	97.4	3232	2	AAX57057	Aax57057 Human KCN
6	2499.4	97.4	3232	10	AAD58489	Aad58489 Human pot
7	2499.4	97.4	3232	13	ADS17844	Ads17844 Human KCN
8	2499	97.4	3232	5	AAS74830	Aas74830 DNA encod
9	2495	97.3	7411	10	ADD29557	Add29557 Human tum
10	2495	97.3	7420	11	ADN38963	Adn38963 Cancer/an
11	2495	97.3	7420	11	ADP65810	Adp65810 Human mRN
12	2495	97.3	7420	11	ADP65731	Adp65731 Human pot
13	2495	97.3	7420	12	ADL06495	Adl06495 Human tum
14	2495	97.3	7863	10	ADJ56529	Adj56529 Human cDN
15	2493.4	97.2	7407	10	ADB78685	Adb78685 Human pot

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2506.4	97.7	4512	15	US-10-084-817-334	Sequence 334, App
2	2499.4	97.4	2619	15	US-10-345-680-18	Sequence 18, Appl
3	2499.4	97.4	3232	15	US-10-345-680-16	Sequence 16, Appl
4	2499.4	97.4	3232	16	US-10-096-578-1	Sequence 1, Appli
5	2499.4	97.4	3232	19	US-10-820-307-1	Sequence 1, Appli
6	2495	97.3	7411	20	US-10-335-053-6	Sequence 6, Appli
7	2495	97.3	7420	17	US-10-295-027-281	Sequence 281, App
8	2495	97.3	7420	20	US-10-643-795A-75	Sequence 75, Appl
9	2495	97.3	7420	21	US-10-948-518-75	Sequence 75, Appl
10	2495	97.3	7863	15	US-10-084-817-335	Sequence 335, App
11	2493.4	97.2	7407	21	US-10-482-834A-54	Sequence 54, Appl
12	2493.4	97.2	7407	21	US-10-482-834A-56	Sequence 56, Appl
13	2493.4	97.2	7407	21	US-10-482-834A-57	Sequence 57, Appl
14	2493.4	97.2	7407	21	US-10-482-834A-58	Sequence 58, Appl
15	2493.4	97.2	7407	21	US-10-482-834A-59	Sequence 59, Appl

SUMMARIES

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Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	757.8	29.5	846	4	BI818397	BI818397 603032857
2	739.4	28.8	864	7	CK772601	CK772601 961159 MA
3	734.4	28.6	1624	3	CR621726	CR621726 full-leng
4	610.4	23.8	920	2	BF317072	BF317072 601903470
5	610.2	23.8	914	2	BF312386	BF312386 601898926
6	605	23.6	634	1	AI589812	AI589812 tm74f08.x
7	600	23.4	600	7	CV029888	CV029888 8836 Full
8	598	23.3	622	2	BE257127	BE257127 601108867
9	579.6	22.6	903	1	AL535991	AL535991 AL535991
10	565	22.0	597	2	BE260338	BE260338 601151405
11	546.2	21.3	1004	5	BQ219245	BQ219245 AGENCOURT
12	531.4	20.7	884	6	CD580227	CD580227 EST_PSF00
13	526.8	20.5	733	5	BU058046	BU058046 UI-M-FOO-
14	515.6	20.1	541	1	AI968605	AI968605 wt90e10.x
15	502.6	19.6	1571	3	AK040190	AK040190 Mus muscu

09/209,125 Results

SEQ ID NO: 3

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4495	100.0	854	2	AAY23215	Aay23215 Human bra
2	4495	100.0	912	4	ABG10644	Abg10644 Novel hum
3	4471	99.5	872	2	AAY08341	Aay08341 Human KCN
4	4471	99.5	872	7	AAE38588	Aae38588 Human pot
5	4471	99.5	872	8	ADM51121	Adh51121 Potassium
6	4471	99.5	872	8	ADM77997	Adm77997 KCNQ2-f1
7	4471	99.5	914	4	ABG10643	Abg10643 Novel hum
8	4463	99.3	872	8	ADS17845	Adis17845 Human KCN
9	4461	99.2	930	2	AAY08347	Aay08347 Human mut
10	4460.5	99.2	871	2	AAY01529	Aay01529 Amino aci
11	4431	98.6	844	5	AAE16619	Aae16619 Human pot
12	4431	98.6	844	7	ADN38964	Adn38964 Cancer/an
13	4431	98.6	844	8	ADL06572	Adl06572 Human tum
14	4426	98.5	844	7	ADB78617	Adb78617 Human pot
15	4410	98.1	842	8	ADS17846	Adis17846 Human KCN

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4471	99.5	872	14	US-10-345-680-17	Sequence 17, Appl
2	4471	99.5	872	14	US-10-096-578-2	Sequence 2, Appl
3	4471	99.5	872	16	US-10-744-796-7	Sequence 7, Appl
4	4463	99.3	872	16	US-10-820-307-2	Sequence 2, Appl
5	4461	99.2	930	14	US-10-096-578-96	Sequence 96, Appl
6	4460.5	99.2	871	13	US-10-128-870-20	Sequence 20, Appl
7	4460.5	99.2	871	14	US-10-131-685-20	Sequence 20, Appl
8	4431	98.6	844	9	US-09-866-020-30	Sequence 30, Appl
9	4431	98.6	844	9	US-09-813-148-4	Sequence 4, Appl
10	4431	98.6	844	9	US-09-810-796-14	Sequence 14, Appl
11	4431	98.6	844	15	US-10-295-027-282	Sequence 282, App
12	4431	98.6	844	16	US-10-661-629-4	Sequence 4, Appl
13	4431	98.6	844	16	US-10-643-795A-152	Sequence 152, App
14	4431	98.6	844	17	US-10-850-928-34	Sequence 34, Appl
15	4431	98.6	844	17	US-10-948-493-29	Sequence 29, Appl

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1959.5	43.6	393	2	JC5275	voltage-gated pota
2	1152	25.6	744	2	T34116	voltage-gated pota
3	838.5	18.7	645	2	T27186	hypothetical prote
4	397	8.8	664	2	T28852	probable potassium
5	310	6.9	613	2	A39402	potassium channel
6	310	6.9	624	2	S22703	voltage-gated pota
7	307	6.8	858	2	S31761	potassium channel
8	305.5	6.8	581	2	S17150	potassium channel
9	291.5	6.5	802	2	JH0595	potassium channel
10	289.5	6.4	853	1	CHRTD1	potassium channel
11	282.5	6.3	857	2	I56529	potassium channel
12	281	6.3	585	2	A39395	delayed rectifier
13	279	6.2	511	2	A46020	potassium channel
14	279	6.2	511	2	S07095	potassium channel
15	275	6.1	769	2	I56546	Shaw type potassi

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	4471	99.5	872	1	CIQ2_HUMAN	O43526 homo sapien
2	4253	94.6	870	2	Q8R498	Q8r498 mus musculu
3	4243	94.4	852	1	CIQ2_RAT	O88943 rattus norv
4	3510	78.1	759	1	CIQ2_MOUSE	Q9z351 mus musculu
5	2009	44.7	409	2	Q9BX08	Q9bx08 homo sapien
6	1932	43.0	363	2	Q9BQU4	Q9bqu4 homo sapien
7	1904	42.4	399	2	Q9BQU5	Q9bqu5 homo sapien
8	1827	40.6	873	1	CIQ3_RAT	O88944 rattus norv
9	1827	40.6	873	2	Q8K3F6	Q8k3f6 mus musculu
10	1823	40.6	872	1	CIQ3_HUMAN	O43525 homo sapien
11	1818	40.4	866	1	CIQ3_BOVIN	P58126 bos taurus
12	1807.5	40.2	897	1	CIQ5_HUMAN	Q9nr82 homo sapien
13	1804.5	40.1	878	1	CIQ5_MOUSE	Q9jk45 mus musculu
14	1791.5	39.9	695	1	CIQ4_HUMAN	P56696 homo sapien
15	1455.5	32.4	296	2	Q6DKP7	Q6dkp7 cavia porce